

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Eaton, Dan L.
DeSauvage, Frederic J.

(ii) TITLE OF INVENTION: MPL LIGAND

10 (iii) NUMBER OF SEQUENCES: 32

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

15 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: patin (Genentech)

20 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/223263
(B) FILING DATE: 4-APR-1994
(C) CLASSIFICATION:

25 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/196689
(B) FILING DATE: 15-FEB-1994

30 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/185607
(B) FILING DATE: 21-JAN-1994

35 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/176553
(B) FILING DATE: 3-JAN-1994

40 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Winter, Daryl B.
(B) REGISTRATION NUMBER: 32,637
(C) REFERENCE/DOCKET NUMBER: 871P3

45 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-1249
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids
5 (B) TYPE: amino acid
(C) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10 Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
1 5 10 15
Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
15 20 25 30
Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
35 40 45
Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
50 55 60
Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
65 70 75
Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
80 85 90
Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
95 100 105
Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
110 115 120
Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
125 130 135
Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
140 145 150
40 Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
155 160 165
Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr
170 175 180
45 Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu
185 190 195
Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser
50 200 205 210

1 Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe
215 220 225
5 Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu
230 235 240
10 Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
245 250 255
15 Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly
260 265 270
20 Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro
275 280 285
25 Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro
290 295 300
30 Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr
305 310 315
35 Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro
320 325 330
40 25 Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His
335 340 345
45 Ser Gln Asn Leu Ser Gln Glu Gly
350 353

30 (2) INFORMATION FOR SEQ ID NO:2:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1795 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCTTCCTTACCCATCTGCTCCCCAGAGGGCTGCCTGCTGTGCACTTGGGTC 50

45 CTGGAGCCCTTCTCCACCCGGATAGATTCCTCACCCCTTGGCCCGCCCTTG 100

CCCCACCCCTA CTCTGCCAGAAGTGCAAGAGCCTAAGCCGCCTCCATGGC 150

50 CCCAGGAAGGATTCAAGGGAGAGGGCCCCAAACAGGGAGGCCACGCCAGCCA 200

20 5
GACACCCCGG CCAGAATGGA GCTGACTGAA TTGCTCCTCG TGGTCATGCT 250
5
TCTCCTAACT GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG 300
10
ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC 350
15
AGACTGAGCC AGTGCCAGA GGTCACCCCT TTGCCTACAC CTGTCCTGCT 400
GCCTGCTGTG GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA 450
25
CCAAGGCACA GGACATTCTG GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG 500
ATGGCAGCAC GGGGACAACG GGGACCCACT TGCCTCTCAT CCCTCCTGGG 550
30
GCAGCTTTCT GGACAGGTCC GTCTCCTCTG TGGGGCCCTG CAGAGCCTCC 600
25
TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC 650
AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT 700
35
CCTGATGCTT GTAGGAGGGT CCACCCCTCTG CGTCAGGCAG GCCCCACCCA 750
CCACAGCTGT CCCCAGCAGA ACCTCTCTAG TCCTCACACT GAACGAGCTC 800
40
CCAAACAGGA CTTCTGGATT GTTGGAGACA AACTTCACTG CCTCAGCCAG 850
TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTGGACCA AATCCCCGGA 900
45
TACCTGAACA GGATACACGA ACTCTTGAAT GGAACTCGTG GACTCTTCC 1000
50
TGGACCCTCA CGCAGGACCC TAGGAGCCCC GGACATTCC TCAGGAACAT 1050
CAGACACAGG CTCCCTGCCA CCCAACCTCC AGCCTGGATA TTCTCCTTCC 1100

5 CCAACCCATC CTCCTACTGG ACAGTATAACG CTCTTCCCTC TTCCACCCAC 1150

10 CTTGCCAGC CCTGTGGTCC AGCTCCACCC CCTGCTTCCT GACCCTTCTG 1200

15 CTCCAACGCC CACCCCTACC AGCCCTCTTC TAAACACATC CTACACCCAC 1250

20 TCCCAGAATC TGTCTCAGGA AGGGTAAGGT TCTCAGACAC TGCCGACATC 1300

25 AGCATTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC CCTGGGAGAC 1350

30 AACTGGACAA GATTCCTAC TTCTCCTGA AACCCAAAGC CCTGGTAAAA 1400

35 GGGATACACA GGACTGAAAA GGGAAATCATT TTTCACTGTA CATTATAAAC 1450

40 CTTCAGAACG TATTTTTTA AGCTATCAGC AATACTCATC AGAGCAGCTA 1500

45 GCTCTTGGT CTATTTCTG CAGAAATTG CAACTCACTG ATTCTCTACA 1550

50 TGCTCTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG CCTGGCAGTT 1600

55 GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA AAGGGTAATT 1650

60 TCCTTGCTT CAAATTCAAG GCCTTCAAC GCCCCCATCC CCTTTACTAT 1700

65 CATTCTCAGT GGGACTCTGA TCCCATATTG TTAACAGATC TTTACTCTTG 1750

70 AGAAATGAAT AAGCTTCTC TCAGAAAAAA AAAAAAAA AAAAA 1795

75 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu
1 5 10 15

5 Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
20 25 30

Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
10 35 40 42

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 390 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCTGG AATACCAGCT GAGAATGATT TCCTCCTCAT CTTTCAACCT 50

25 CACCTCTCCT CATCTAAGAA TTGCTCCTCG TGGTCATGCT TCTCCTAACT 100

30 GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG ACCTCCGAGT 150

CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC AGACTGGTGA 200

35 GAACTCCCAA CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA 250

CTCCCAGGAA GACACCATCA CTTCCCTCTAA CTCCTTGACC CAATGACTAT 300

40 TCTTCCCATA TTGTCCCCAC CTACTGATCA CACTCTCTGA CAAGAATTAT 350

45 TCTTCACAAT ACAGCCCGCA TTAAAAGCT CTCGTCTAGA 390

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTAAGGACC TTATGGT~~CGA~~ CTGTTACTAA AGGAGGAGTA GAAAGTTGGA 50
GTGGAGAGGA GTAGATTCTT AACGAGGAGC ACCAGTACGA AGAGGATTGA 100
CGTTCCGATT GCGACAGGTC GGGCCGAGGA GGACGAACAC TGGAGGCTCA 150
GGAGTCATTT GACGAAGCAC TGAGGGTACA GGAAGTGT~~CG~~ TCTGACCACT 200
CTTGAGGGTT GTAATAGGGG AAATAGGCC~~C~~ ATTGACCATT CTGTGGGTAT 250
GAGGGTC~~CTT~~ CTGTGGTAGT GAAGGAGATT GAGGA~~ACT~~GG GTTACTGATA 300
AGAAGGGTAT AACAGGGGTG GATGACTAGT GTGAGAGACT GTTCTTAATA 350
AGAAGTGT~~A~~ TGTCGGCGT AAATTT~~CG~~A GAGCAGATCT 390

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
1 5 10 15
Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro
20 25 30

1 Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp
35 40 45

5 Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala
50 55 60

10 Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met
65 70 75

15 Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu
80 85 90

20 Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
95 100 105

25 Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala
110 115 120

30 His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu
125 130 135

35 Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu
140 145 150

40 Cys Val Arg Arg Ala Pro Pro Thr Thr Ala Val Pro Ser Arg Thr
155 160 165

45 Ser Leu Val Leu Thr Leu Asn Glu Leu Pro Asn Arg Thr Ser Gly
170 175 180

50 Leu Leu Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr Thr Gly Ser
185 190 195

55 Gly Leu Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile Pro Gly
200 205 210

60 Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly Tyr
215 220 225

65 Leu Asn Arg Ile His Glu Leu Leu Asn Gly Thr Arg Gly Leu Phe
230 235 240

70 Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro Asp Ile Ser Ser
245 250 255

75 Gly Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly
260 265 270

80 Tyr Ser Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu
275 280 285

Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu His
290 295 300
5 Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser
305 310 315
Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln
320 325 330
10 Glu Gly
332

(2) INFORMATION FOR SEQ ID NO:7:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr
1 5 10 15
Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala
20 25 30
Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
35 40 45
30 Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala
50 55 60
Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu
35 65 70 75
Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro
80 85 90
40 Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
95 100 105
Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser
110 115 120
45 Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala
125 130 135
Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg
50 140 145 150

Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
155 160 165

5 Arg
166

(2) INFORMATION FOR SEQ ID NO:8:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTCCTTGG CCCACCTCTC TCCCACCCGA CTCTGCCGAA AGAACACAG 50

20 AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAAGGG GAGAGGCC 100

25 ATACAGGGAG CCACCTTCAGT TAGACACCTT GGCCAGAAATG GAGCTGACTG 150

30 ATTTGCTCCT GGCAGCCATG CTTCTTGAG TGGAAGACT AACTCTGTCC 200

AGCCCCGTAG CTCCTGCCTG TGACCCCAGA CTCTAAATA AACTGCTGCG 250

TGACTCCCAC CTCCTTCACA GCCGACTGAG TCAGTGTCCC GACGTCGACC 300

35 CTTTGTCTAT CCCTGTTCTG CTGCCTGCTG TGGACTTTAG CCTGGGAGAA 350

40 TGGAAAACCC AGACGGAACA GAGCAAGGCA CAGGACATTG TAGGGGCAGT 400

GTCCCTTCTA CTGGAGGGAG TGATGGCAGC ACGAGGACAG TTGGAACCT 450

45 CCTGCCTCTC ATCCCTCCTG GGACAGCTT CTGGCAGGT TCGCCTCCTC 500

50 TTGGGGGCCCT TGCAGGGCCT CCTAGGAACC CAGGGCAGGA CCACAGCTCA 550

CAAGGACCCCC AATGCCCTCT TCTTGAGCTT GCAACAACTG CTTCGGGGAA 600

AGGTGCGCTT CCTGCTTCTG GTAGAAGGTC CCACCCCTCTG TGTCAGACGG 650
5
ACCCCTGCCAA CCACAGCTGT CCCAAGCAGT ACTTCTCAAC TCCTCACACT 700
AAACAAGTTC CCAAACAGGA CTTCTGGATT GTTGGAGACG AACTTCAGTG 750
10 TCACAGCCAG AACTGCTGGC CCTGGACTTC TGAGCAGGCT TCAGGGATTC 800
AGAGTCAAGA TTACTCCTGG TCAGCTAAAT CAAACCTCCA GGTCCCCAGT 850
15 CCAAATCTCT GGATACCTGA AGAGGACACA CGGACCTGTG AATGGAACTC 900
ATGGGCTCTT TGCTGGAACC TCACTTCAGA CCCTGGAAGC CTCAGACATC 950
20 TCGCCCGGAG CTTTCAACAA AGGCTCCCTG GCATTCAACC TCCAGGGTGG 1000
25 ACTTCCTCCT TCTCCAAGCC TTGCTCCTGA TGGACACACA CCCTTCCCTC 1050
CTTCACCTGC CTTGCCACC ACCCATGGAT CTCCACCCCA GCTCCACCC 1100
30 CTGTTTCCTG ACCCTTCCAC CACCATGCCT AACTCTACCG CCCCTCATCC 1150
AGTCACAATG TACCCCTCATC CCAGGAATT GTCTCAGGAA ACATAGCGCG 1200
35 GGCACTGGCC CAGTGAGCGT CTGCAGCTTC TCTCGGGGAC AAGCTTCCCC 1250
40 AGGAAGGCTG AGAGGCAGCT GCATCTGCTC CAGATGTTCT GCTTCACCT 1300
AAAAGGCCCT GGGGAAGGGA TACACAGCAC TGGAGATTGT AAAATTTAG 1350
45 GAGCTATTTT TTTTTAACCT ATCAGCAATA TTCATCAGAG CAGCTAGCGA 1400
50 TCTTTGGTCT ATTTTCGGTA TAAATTGAA AATCACTAAT TCT 1443

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 356 amino acids
5 (B) TYPE: amino acid
(C) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

10 Met Glu Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu Ala Val
1 5 10 15

15 Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys Asp Pro
20 25 30

20 Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His Leu Leu His Ser
35 40 45

25 Arg Leu Ser Gln Cys Pro Asp Val Asp Pro Leu Ser Ile Pro Val
50 55 60

30 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
65 70 75

35 Thr Glu Gln Ser Lys Ala Gln Asp Ile Leu Gly Ala Val Ser Leu
80 85 90

40 Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser
95 100 105

45 Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
110 115 120

50 Leu Leu Gly Ala Leu Gln Gly Leu Leu Gly Thr Gln Leu Pro Leu
125 130 135

55 Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Leu Phe Leu
140 145 150

60 Ser Leu Gln Gln Leu Leu Arg Gly Lys Val Arg Phe Leu Leu Leu
155 160 165

65 Val Glu Gly Pro Thr Leu Cys Val Arg Arg Thr Leu Pro Thr Thr
170 175 180

70 Ala Val Pro Ser Ser Thr Ser Gln Leu Leu Thr Leu Asn Lys Phe
185 190 195

75 Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Ser Val Thr
200 205 210

1 Ala Arg Thr Ala Gly Pro Gly Leu Leu Ser Arg Leu Gln Gly Phe
 215 220 225
 5 Arg Val Lys Ile Thr Pro Gly Gln Leu Asn Gln Thr Ser Arg Ser
 230 235 240
 Pro Val Gln Ile Ser Gly Tyr Leu Asn Arg Thr His Gly Pro Val
 245 250 255
 10 Asn Gly Thr His Gly Leu Phe Ala Gly Thr Ser Leu Gln Thr Leu
 260 265 270
 15 Glu Ala Ser Asp Ile Ser Pro Gly Ala Phe Asn Lys Gly Ser Leu
 275 280 285
 Ala Phe Asn Leu Gln Gly Gly Leu Pro Pro Ser Pro Ser Leu Ala
 290 295 300
 20 Pro Asp Gly His Thr Pro Phe Pro Pro Ser Pro Ala Leu Pro Thr
 305 310 315
 Thr His Gly Ser Pro Pro Gln Leu His Pro Leu Phe Pro Asp Pro
 320 325 330
 25 Ser Thr Thr Met Pro Asn Ser Thr Ala Pro His Pro Val Thr Met
 335 340 345
 Tyr Pro His Pro Arg Asn Leu Ser Gln Glu Thr
 350 355 356

30 (2) INFORMATION FOR SEQ ID NO:10:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 amino acids
 (B) TYPE: amino acid
 (C) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ser Pro Val Ala Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
 1 5 10 15
 Leu Arg Asp Ser His Leu Leu His Ser Arg Leu Ser Gln Cys Pro
 20 25 30
 45 Asp Val Asp Pro Leu Ser Ile Pro Val Leu Leu Pro Ala Val Asp
 35 40 45
 Phe Ser Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Ser Lys Ala
 50 55 60

Glh Asp Ile Leu Gly Ala Val Ser Leu Leu Leu Glu Gly Val Met
65 70 75

5 Ala Ala Arg Gly Gln Leu Glu Pro Ser Cys Leu Ser Ser Leu Leu
80 85 90

Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
95 100 105

10 Gly Leu Leu Gly Thr Gln Gly Arg Thr Thr Ala His Lys Asp Pro
110 115 120

Asn Ala Leu Phe Leu Ser Leu Gln Gln Leu Leu Arg Gly Lys Val
125 130 135

15 Arg Phe Leu Leu Leu Val Glu Gly Pro Thr Leu Cys Val Arg Arg
140 145 150

20 Thr Leu Pro Thr Thr Ala Val Pro Ser Ser Thr Ser Gln Leu Leu
155 160 165

Thr Leu Asn Lys Phe Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr
170 175 180

25 Asn Phe Ser Val Thr Ala Arg Thr Ala Gly Pro Gly Leu Leu Ser
185 190 195

Arg Leu Gln Gly Phe Arg Val Lys Ile Thr Pro Gly Gln Leu Asn
200 205 210

30 Gln Thr Ser Arg Ser Pro Val Gln Ile Ser Gly Tyr Leu Asn Arg
215 220 225

35 Thr His Gly Pro Val Asn Gly Thr His Gly Leu Phe Ala Gly Thr
230 235 240

Ser Leu Gln Thr Leu Glu Ala Ser Asp Ile Ser Pro Gly Ala Phe
245 250 255

40 Asn Lys Gly Ser Leu Ala Phe Asn Leu Gln Gly Gly Leu Pro Pro
260 265 270

Ser Pro Ser Leu Ala Pro Asp Gly His Thr Pro Phe Pro Pro Ser
275 280 285

45 Pro Ala Leu Pro Thr Thr His Gly Ser Pro Pro Gln Leu His Pro
290 295 300

50 Leu Phe Pro Asp Pro Ser Thr Thr Met Pro Asn Ser Thr Ala Pro
305 310 315

His Pro Val Thr Met Tyr Pro His Pro Arg Asn Leu Ser Gln Glu
320 325 330

5 Thr
331

(2) INFORMATION FOR SEQ ID NO:11:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

20 Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

25 Leu Arg Asp Asp His Ser Val Leu His Gly Arg Leu
20 25 27

(2) INFORMATION FOR SEQ ID NO:12:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

40 Ser Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

45 Leu Arg Asp Asp His Val Leu His Gly Arg
20 25

(2) INFORMATION FOR SEQ ID NO:13:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

50 Xaa Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Xaa Asn Lys
1 5 10 14

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

10 Pro Arg Leu Leu Asn Lys Leu Leu Arg
1 5 9

(2) INFORMATION FOR SEQ ID NO:15:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

20 GCCGTGAAGG ACGTGGTCGT CACGAAGCAG TTTATTTAGG AGTCG 45
25

(2) INFORMATION FOR SEQ ID NO:16:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

40 CCNGCNCCNC CNGCNTGYGA 20

(2) INFORMATION FOR SEQ ID NO:17:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

NCCRTGNARN ACRTGRTCRT C 21

5

(2) INFORMATION FOR SEQ ID NO:18:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

20

CCAGCGCCGC CAGCCTGTGA CCCCCGACTC CTAAATAAAC TGCCTCGTGA 50

TGACCACGTT CAGCACGGC 69

25

(2) INFORMATION FOR SEQ ID NO:19:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

35

GGTCGCGGCG GTCGGACACT GGGGGCTGAG GATTTATTTG ACGGAGCACT 50

40

ACTGGTGCAA GTCGTGCCG 69

45

(2) INFORMATION FOR SEQ ID NO:20:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

5 CCAGCACCTC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50

CGACCACGTC TATCACGGC 69

10

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

25 GGTCGTGGAG GCCGTACACT GGGGGCTGAG GATTTATTTG ACGAAGCACT 50

30 GCTGGTGCAG GTAGTGCCG 69

(2) INFORMATION FOR SEQ ID NO:22:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

45 CCAGCACCGC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50

CGATCATGTC TATCACGGT 69

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGTCGTGGCG GCCGTACACT GGGGGCTGAG GATTTATTTG ACGAAGCACT 50

15 GCTAGTACAG ATAGTGCCA 69

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

30 GCTAGCTCTA GAAATTGCTC CTCGTGGTCA TGCTTCT 37

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

45 CAGTCTGCCG TGAAGGACAT GG 22

5 (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

15 Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
1 5 10 15
Leu Arg Asp Ser His Val Leu His
20 23

15 (2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

25 Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro
1 5 10 15
Val Leu Leu Pro Ala Val Asp Phe
20 23

30 (2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

40 Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln
1 5 10 15
Asp Ile Leu Gly Ala Val Thr Leu
20 23

45 (2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
1 5 10 15
5 Cys Leu Ser Ser Leu
20

10 (2) INFORMATION FOR SEQ ID NO:30:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Gly Ala Leu
1 5 10 15
30 Gln Ser Leu
18

(2) INFORMATION FOR SEQ ID NO:31:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys
1 5 10 15
35 Asp Pro Asn Ala Ile Phe
20 21

40 (2) INFORMATION FOR SEQ ID NO:32:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met
1 5 10 15
50 Leu Val Gly Gly Ser Thr Leu Cys Val Arg
20 25